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FIG. 1(1)

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FIG. 1(2)

Trans-
membrane

FIG. 1(3)

2581 861	tacctctgcgaaggggacagagtcccttatcagacaggacagctgcacccagccatcagg Y L C E G T E S P Y Q T G Q L H P A I R	2640 880
2641 881	gtggccgacttaactgcagcacattaacccatgaagacatcagacagctatgggttcaa V A D L L Q H I N L M K T S D S Y G F K	2700 900
2701 901	gaggaatacagagagCttcttgaaggccagtccgttggatgtggctaaaaggat E E Y E S F F E G Q S A S W D V A K K D	2760 920
PTPase Domain I	2761 caaaacagacaaqaacccatacgaaacattatcgatcatgtactccagactcatc 921 Q N R A K [N R Y G N I I A Y D H S R V I	2820 940
	2821 ctgcaacctgtggaaatgacccttcttcsgattacattaatgcacaactacatcgacatt 941 L Q P V E D D F S S D Y I N A N Y I D I	2880 960
2881 961	tggctgtacaggatggcttaccagagaccacactatGGcaactcaaggccagtt W L Y R D G Y Q R P S H Y I A T Q G P V	2940 980
2941 981	catgaaacccgtatatatgtatGGAggatgtgtggcaagacagactctgttattgt H E T V Y D F W R M V W Q E Q S A C I V	3000 1000
3001 1001	atggtcactaaTtttgtGaaatTGGCGGgtgtataatattggctgtatgtat M V T N L V E V G R V K C Y K Y W P D D	3060 1020
3061 1021	actgggttatgttgacttcaagtcacCCGgttagaaatggagccacttgtgtat T E V Y G D F K V T C V E M E P L A E Y	3120 1040
3121 1041	gtcgtaggacattcaccttggaaaggaggggctataatgaaatccgtgaagtcaaacag V V R T F T L E R G Y N E I R E V K Q	3180 1060
3181 1061	ttccacttactggctggccgtaccatgtttccatcacacgcacaggctctgtca F H F T G W P D H G V P Y H A T G L L S	3240 1080
3241 1081	tttatccggaggtcaagctatctaaccctcccaatgtgtggccatgtgtactgc F I R R V K L S N P P S A G P I V V H C	3300 1100
3301 1101	agtgtgtgtctggcgacacggctgttacattgttattgcataatgtggacatggct S A G A G R T G C Y I V I D I M L D M A	3360 1120
3361 1121	gaaagagaggggtgtgttgcataactcataactgtgtgaaaggcttacgtctggcgcat E R E G V V D I Y N C V K A L R S R R I	3420 1140
3421 1141	aatatggatcacagacaggacagactacatttttattcatgtgcattttagaagctgc N M V Q T E E Q Y I F I H D A I L E] A C	3480 1160

FIG. 1(4)

FIG. 1(5)

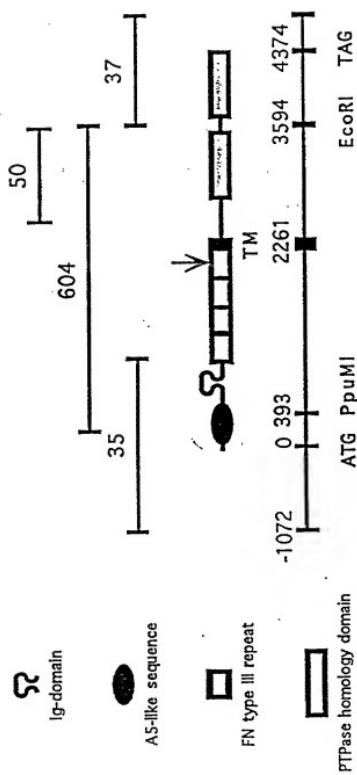


FIG. 2

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FIG. 3

I (296) * PQL L GVGPTVLLQIANS I IGDPILLKEW V RMTSGSKTEPHAVNA PTKLWHLDPTE. YEVIRVLL T R PG EG G TGLPGPPLITRT
II (392) P .KTP L KIABIGA. RRIAVD W ESLGYNWTRCHT P NYTICHYFRGHINBSRADCLDMDPKA... .POHVYNNH L P PY TN V SLXHML.TNPEG
III (493) P VKS L QCTSF... .NKTFLN W KEPLNGGITQ Y EVSYSRSRSFDPAVVAG PFCOTVSNMNSPHYFEMH L H PG TT Y QFFIRASVTKSF
IV (596) P DVE G VDASLMEANTTIVL L RPADAKARISA Y QIVBQUMPHRTER. EAGAMECYOV.... .PVYTONA L S GA AP Y YFAEELUPCNLP
PBN-III(7) P PPN L HLEANPDT. GVLYWS W ERSTPD.. ITG Y RITTPTINGQOONSLEEVHADQ..... .SSCTFDN L S PG LE Y NVSVY.. .TVKDD

FIG. 4

PTP-X (34)	GGCTFDQGAGDYHODLYDDPEKMYVSAQE
PTP-μ (26)	PHYLIPPEMPGISMVYDSSNNHDPEKEARLQLPTMKEN
A5 (651)	DTHCICIDFSYLLYSOK
Consensus	GGCLPDEPVSTGYSQADEDDEWEQVNTLIRKPT

.

PTP-X (34)	CKFGNQSOQTIVENKWHQDTSIISLAKWAVANASKTGP..
PTP-μ (26)	VQDHTGDDONFTYSSADERHETRAALASPVYSSRISACILTYWYIM..
A5 (651)
Consensus	D--D--W--N--T--P--.

.

PTP-X	GLNPCTNLILYRVN
PTP-μ	KGPLANPIINNTGFTGRDMRLRAELNSTWPNEQVIFERATVSGGRGSCYIAIDDIQVLSY
A5	NAAPGLLANYVVKVN
Consensus	NGPIGNPNTNNSCDPRTWIRALEAISTFWPNPYQVITEV

.

PTP-X	GSHVGTLSIKLVENEEEDFQTLWVTSNGQDQWKEAVRVVHLHKHQ
PTP-μ	YQVIVECVWVGKSAGGIAVDDIIAH
A5
Consensus	G---GTL-I-K---W-VSG---G---W-A---.

.

FIG. 5

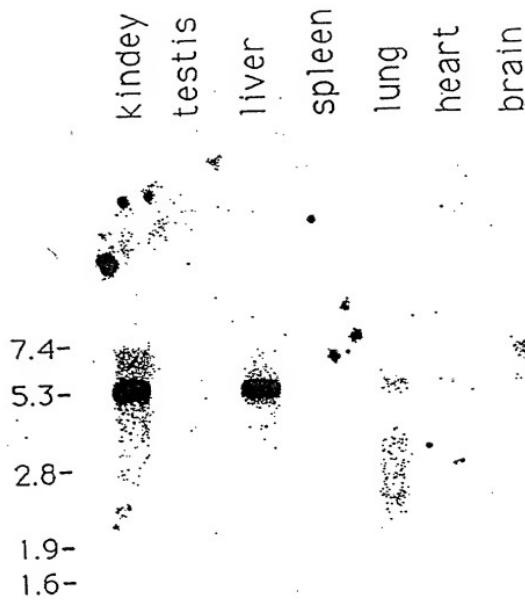


FIG. 6

Transfected:	-	-	-	+	+	+
Antibody:	pre	α -K	α -K	pre	α -K	α -K
Peptide:	-	-	+	-	-	+

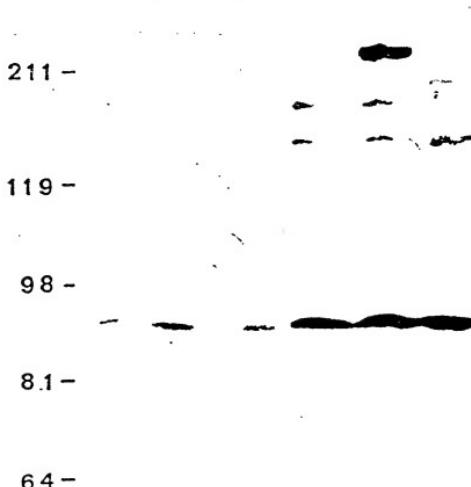
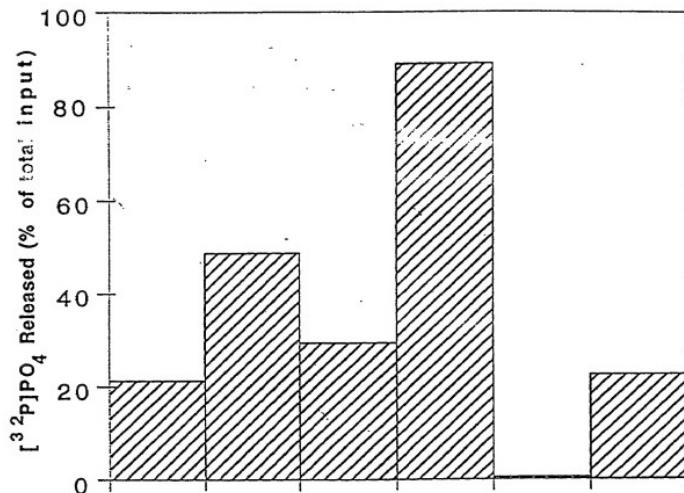


FIG. 7



Transfection	mock	κ	mock	κ	mock	κ
Antibody	pre	pre	116	116	116	116
Vanadate	-	-	-	-	+	+

FIG. 8

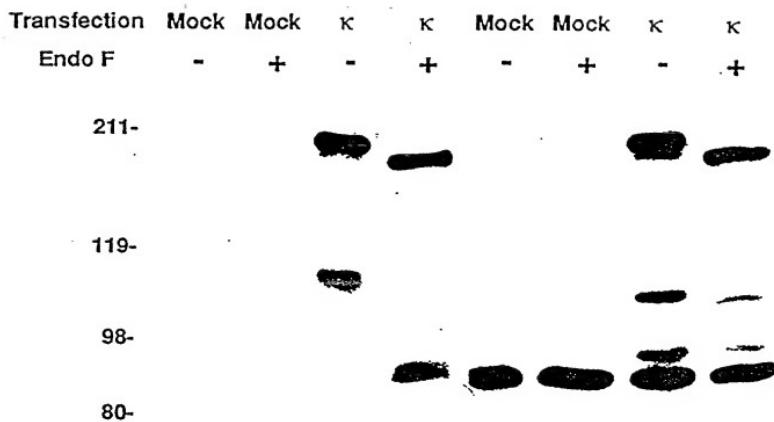


FIG. 9

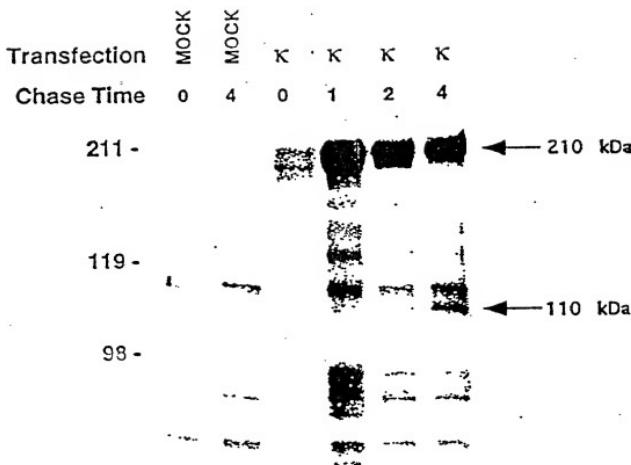


FIG. 10

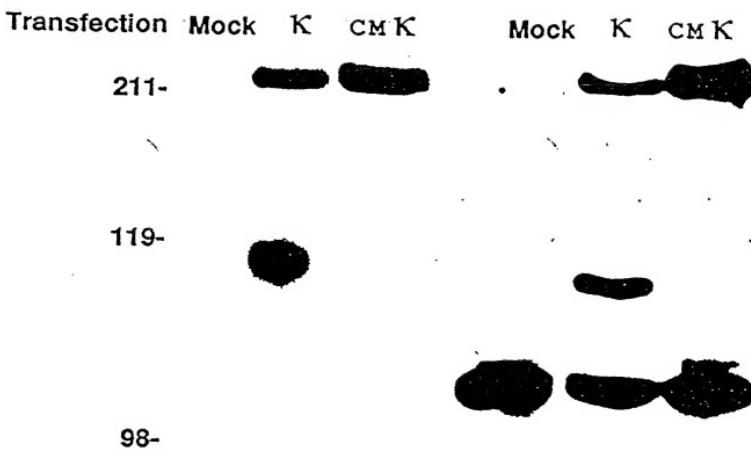


FIG. 11

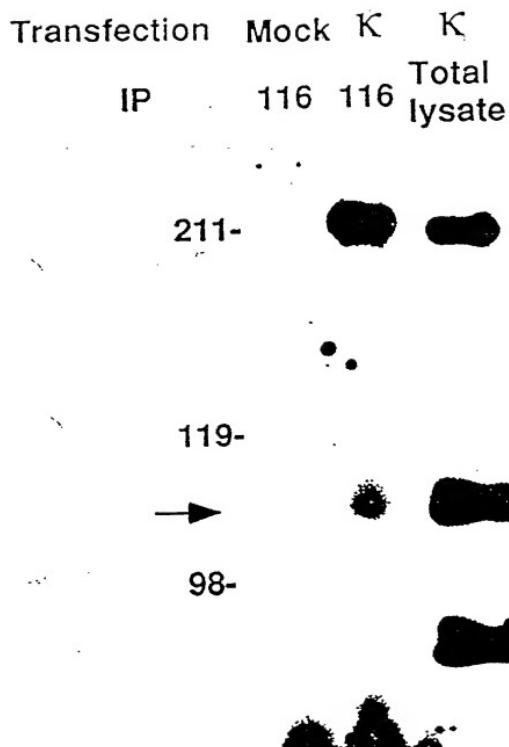


FIG. 12

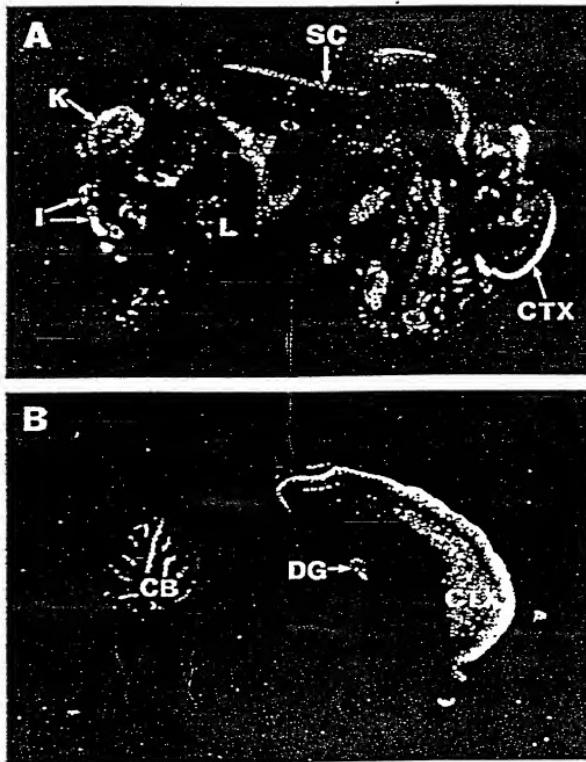


FIG. 13

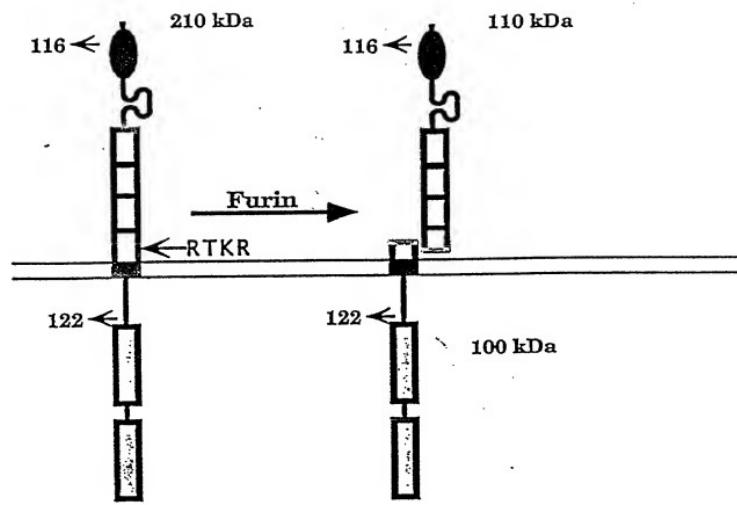


FIG. 14

1 ATGGATACCGACTCCGGCGGCCGCTGCCCTCTTGTGGCCTCTTGCGCCTCTTCCTGGCCTCTCCCTGGATAGGC
 -1 M D T T A A A L P A F V A L L L S P W P L L G S A 80
 27 Q C Q F S A G G C T F D D G P G A C D Y H Q D L Y D D 53
 161 ACTTTGAATGGGTCGCACTGGTACTGCTOAAGGCTCATATCTACCAACCCGAGATGCCCAAGGTTCTATATGATAGT 240
 54 F E W V E V S A Q E F H Y L P P E M P Q G S Y M X V 80
 241 GACTCTCAGATCACGACCCCTGGAGAAAAAGCCAGACTTCAGCTGCCATCAAATGARGAGAACGACACTACTGCATTGA 320
 61 D S S D H D P G E K A R L Q L P T M K E N D T H C I D 107
 321 TTTCAGTACCTATTATAGGCCAGAAGGACTCTGACTCTGGCCTTGGAGACATATTAGTTAGGGTGATAAAGGACCTC 400
 107 F S Y L L Y S Q K G L N P G T L T N L V R V N K G P L 133
 401 TTGCAATCTCAATTGGAAATGGTACTGATTCAGCGTAGAGATTGGCTTCGGGCTGACTAGCAGTGACCCATTNG 480
 134 A N P I W N V T G F T G R D W L R A E L A V S T F W 160
 481 CCCAAATTAATCAGGTAATTGGAGCTGAAGTCAGGAGACTCTGACTAGGAGAAGTGGTTATATTGCCATTGATGACATCCAAGT 560
 161 P M E Y Q V I F P E A V S G R G S Y I A I D D I Q V 187
 561 ACTGAGTTATCTTGATATACTCTCATTCCTCTGGCTCTAGGGCATGAGGTGATAGGCAAGGGAAAAGCTACAT 640
 187 L S Y P C D K S P H F L R L G D V E V N A G Q N A T F 213
 641 TTCACTGCTTGGCAAGGGAGAGATGCTGTCATAACAGATTAGGCTCAGAGGAAATGGAGAAGATACCAAGTA 720
 214 Q C I A T G R D V A H N K L Q R R N G E D T F V 240
 721 GCCCAAGACTAAAGACATCAATCATAGAAGGTTGGCCCTTCCTGAGATTGCAAGAACGTGACAAAGACTGACCAAGGATT 800
 241 A Q T K N I N H E R R F A S F R L Q E V T K T D Q D L 267
 801 GTATGCCCTGTTGACTCAGTCAGAACAGGAGATGCTGTCATAACAGATTAGGCTCAGAGGAAATGGAGAAGATACCAAGTA 880
 267 Y R C T Q S E R G S G V S N F A Q O L I V R E P P R P 293
 881 CCATTGCTCTCTCAGGTTCTGGTTGGGCTACATATTGGCTGATCACAATTAGGCAACTAAATGGCACTGATCATTGGCAT 960
 294 I A A P P Q L L G V G P T Y L L I Q L N A N S I I G D 320
 961 GGTCCTATCTCATCTGAAAGAGAGTAAAGACTCGGAACGATCATCGAGTCTGGCAAGAAACCCATCGACTAACTCCAAAC 1040
 321 G P I X I L K E V E Y R M T S G S W T E T H A V N A P T 347
 1041 TTACAAATTATGGCATTAGATCAGATCCGAAATATGAGATCCGAGTTCTACTTACAAAGRCTGGTAAAGCTGGAAACCG 1120
 347 Y K L W H L D P D T E Y E I R V L L T R P G E G G G T G 373
 1121 GGCTCCCAAGGACCTCCACTAAATCACCAGAACAAAATGGCAGAACCTGAGAACCTAACAGAACATTAAGATTGCTGAA 1200
 374 L P G P P L I T T R T K C A E P M R T F P K T L K I A E 400
 1201 ATACAGGCAAGACGGATTGCTGGACTGGAAATcCTGGGTTAACACATTACGCGTGGCCACACTTTAAATGTCAGT 1280
 401 I X Q A R R I A V D W E S L G Y N I T R C H T F N V T I 427
 1281 CTGGTACCACTTCTGCTGGTACACAGAACGAGCCAGACTGTTGGACATGAGCCCCAAAGGCCCTACOCATGTTG 1360
 427 C Y H Y F R G H N E S K A D C L D M D P K A P Q H V V 453
 1361 TGAACTCTGCCACCTTATACAAATGTCAGCTGCCAGATGATCTAACCAATCCAGAGGGAAAGGAGACTGAGAG 1440
 454 N H L P F Y T N V S L K M I L T N P E G R K E S E E 480
 1441 ACAATTATTCACACTGATGAGAGATGCTGCCCTGGTCCCCTGACCTGATCAAATCTCTCAAGGAACATCCTTTGAAAATAGAT 1520
 461 T I I Q T D E D V P V P V K S L O G G T S F E N K I 507
 1521 CTTCCTGAACTGGAAAGAACCTTGGATCAAATGGAAATCATCACTCAATATGAGATCAGGTATAGCTAGTAAAGATCAT 1600
 507 F L N N W K E P L D P N G I I T Q Y I S Y S S I R S F 533
 1601 TTGATCTGCACTGGCACTGGGACTCTCCAGACTGATCAAATTTATGGAACTACAGACATCACCCATAGTCTTTATGCGAT 1680
 534 D P A V P V A G P Q T V T S N L W N S T H H V F M H 560
 1681 CTCCACCTGGAAACGAGCTTACAGTTCTATCAAGAGGCCAGCACGGCTAACAGGCTTGGCTCAGGCCACAGGCCATCAATGT 1760
 561 L H P G T T Y Q F F I R A S T V K G F G P A T A I N V 587
 1761 CACCAACCAATATCTCAGCTCAAACCTTACCTGACTATGAGAGGAGTTGATGCCCTCTCTCAATGAAACTGGCACCACAAATA 1840
 567 T T N I S A F T L P D Y E G V D A S L N E T A T T I T 613
 1841 CTGTATTGAGACGAGCACAAAGCCAAAGGTCCTCTACTGCTCTATGAGATTTGTTGGAGAAGACTGACCCACAC 1920
 614 V L L R P A Q A K G A P I S A Y Q I V V E E L H P H 640

Fig. 15(1)

1921	CGAACCAAGAGAGAAGCCGGAGCCA	TGAAATGCTACCCAGGTTCCTGTCACATA	ACCAAAATGCCATGAGTGGGGGTCACC	2000
641	R T K R E A G A M E C Y Q V P V T Y Q N A M S G G A P			667
2001	GTATTACTTGGCTGCAGAACTACCCCGGGAAACCTACCTGAGCCCTGCCCGGTTCACTGGGGTGACAATCGGACCTACC			2080
667	Y Y F A A E L P P G N L P E P A P F T V G D N R T Y Q			693
2081	AAGGCTTTGGAACCTCCTTGGCTCCGCCAAGGATAACACATCTATTTCCAGGGATGAGCAGTGTGGAGAARGGA			2160
694	G F W N P P L A P R K G Y N I Y F Q A M S S V E K E			720
2161	ACTAAAACCCAGTGGCTAACGCTAACAGTACAAAGCAGAACAGAAGAACAGAGACTGATCCCAGATCCGCCAAGCAGAC			2240
721	T K T C V R I A T K A A T E E P E V I P D F A Q K T			747
2241	AGACAGACTGGTGAAGAATAGCAGGAATTAGTGTCTGGAAATTGGTGTCTACCTCCTCTCTAGTGTCAATTAAITG			2320
747	D R V V K T I A G I S A G I L V F I L L L V V I L I V			773
2221	TAAAAAGGACCAAACCTTCCAAAAGGCAAAAGGCTACGGGAAATACCCGGCAGAGATGACTCACATGGTGAATGCA			2400
774	K K S K L A K A K R K D A M G N T R Q E M T H V V N A			800
2401	ATGGATCGAAGTATGCTGATCAGGACTCTGCTGAGAGATCTCTTCCATCACCTTCAGGACCAACATACT			2480
801	M D R S Y A D Q S T L H A E D P L S I T F M D Q H N F			827
2481	TAGTCCAGATATGAGAACCAAGCTCTGAGCAGACTGAGTGTGGCTTCTAGACGCTACCCCTGTGAGGGAA			2560
827	S P R H N S A T A E S S R L L D V F R Y L C E G T			853
2561	CGGACATCCCTTACCAAGACAGCCTACCTCACAGCTACGGCTACGCTATTACCTGAGGACATTAACCTGAGG			2640
854	E S P Y Q T G Q L H F A I R V A D L L Q B I N L M K			880
2641	ACATCAGACAGCTATGGCTTCAAGGAGGAAATAGAGGAGCTTTTGGAGGACAGTCAGCATCTGGATOTAGCTAAA			2720
881	T S D S Y G K E E Y E S F F E G Q S A S W D V A K K			907
2721	AGATCAAAATAGCAGAACCAAGGATATGGAAACATATAGCATATGATCACTCCAGAGTGATTTGGAAACCCGTAGG			2800
907	D Q N H R A K N R Y G N I X A Y D H S R V I L Q F V E D			933
2801	ATGATCCCTCCAGATTATTAATGCAACTATATTGATGGCTACCGAGACCAAGTCATTACATGCCAACCAAAGGT			2880
934	P F S S D Y I N A N Y I D G Y Q R P S H Y I A T Q G			960
2881	CCCGTTCAAGAACACTGGATGATTCTGGAGGATGATTGGCAAGAACATCTGCTTGATTGTGATGGTTACAAATT			2960
961	P V H E T V Y D F W R M I I W Q E Q S A C I V M V T N L			987
2961	AGTTGAGCTGGCCGGTTAAAGCTATAAATGGCCCTGATGATGACTCTGGCTTTATGGTCAAACTGAGTGTG			3040
987	V E V G R V K C Y K W D P D T E V I G D F K V T C V			1013
3041	TAGAAATGGAACCAACTGGCTGATATGAGTGTGGACATTCACCCCTGGAAAGGGGGGTACATGAAATCCGTGAAGTT			3120
1014	E M P L A E Y V V W R T F T L Z R R G Y N E I R E V			1040
3121	AAACAGTTCATTTCACGGCTGGCTGACCTGGAGTGGCTTACCATGTCACAGGGCTGCTTCTTTATCCGGCAGT			3200
1041	K Q F H F T G W F D H G V P Y H A T G T L L S F I R R V			1067
3201	CAAGTTACAAACCTCCAGCTGGCCCATCTGGTGTACATGGCTGAGCTGGCTGGACCAACTGGCTGCTACATC			3280
1067	K L S N A C P P C G I V V H C S A G A G R T V C I Y V			1093
3281	TGATTGACATCATGCTAGACATGGCTAAAGGAGGGTGTGGTGTATTTACATTGTCAGGCTTAAAGCCTTAAAGCTCG			3360
1094	I D I M L D M A E R E G V V D I X Y N C V K A L R S R			1120
3361	CGTATTAATGGTCAGACAGGAGAACAGTACATTTTATTCATGATGCCATTAGGCTGCTTATGTGAGAAC			3440
1121	R I X M V Q T E E Q Y I F I H D A I L E A C L C G E T			1147
3441	TGCCCCATCTGCTGTAATTAAAGCTGCATATTGGTATGATGAGAATAGACTCCGAGACTACCTCTCCACATCA			3520
1147	A I P V C E F K A A Y F D M I R I D S Q T N S S H L K			1173
3521	AGCATGAATTTCAGACTGAGATTCACTGACCCCTGACTACAGCTGGAGACTGAGCTGAGCTGAGCTGGCCAGAAC			3600
1174	D E F Q T L N S V T P R L Q A E D C S I A C L P R N			1200
3601	CATGACAAAGAACCGTTTCATGGACATGCTGCCACTGACAGATGTCCTGGCTTTTAAATCACATTGAGGGAGACAG			3680
1201	H D K N R F M D M L P P F D R C L C L P F L I T I D G E S S			1227
3681	TAACATACATAGCTGCTTATGGAGACTGGCAACAGCTACAGCTGGCTTACAGCTGGCCATGCCAACAA			3760
1227	N Y A A L H M D S Y R Q F A C C A F V T Q Y P L F N T			1253
3761	CTGAAAAGACTTCGGAGATAGTGTATGTTAGGCTGTAACCTCATTGATGTTAACAGACTGACTGTCCAG			3840
1254	V K D F H R L V Y D Y G C T S I V M L N E V D L S Q			1280

FIG. 15(2)

3841 GGCTGCCCTCAGTACTGGCCAGAGGAAGGGATGCTACGGATAATGCCCAACTGGAATGTATGCTTGTCAATGGA 3920
 1281 G C P Q Y W F E G M L R Y G P I Q V E C H S C S M D 1307

 3921 CTGTGATGTGATCAA CGGATT TTAGGATATGC AATCTAACAGCACACAGAAGGTTATCTGATGCTGAAAGTTTC 4000
 1307 C D V I N R I F R I C N L T R F Q E G Y L M V Q Q F Q 1333

 4001 AGTACCTAGGATGGCTTCTCATCGAAGGATGCCGATCTGATCCAAAGGTCATCTTGAAACTGATACTTCAGGTGGAAAG 4080
 1334 Y L G W A S H R E V P G S K R S F L K L I L Q V E K 1360

 4081 TGGCAGGAGGAATGGCAGGAAGGGAAAGGCCGACGATTATCCACTGCCTAAATGTTGGCGGGCGAAGTGGCATGTTCTG 4160
 1361 W Q E E C E E G E G R T I I H C L N G G R S G M F C 1387

 4161 TGCTATAGGATCGTTGTAATGTTGAAACCGGCAAAATGTTGTCATTTTCATGCACTAAAGACACTGAGGAACA 4240
 1387 A I G I V V E M V K R Q N V V D V F H A V K T L K N S 1413

 4241 GCAAGCCAACATGTTGAGGCCCGAGCAATACCGTTCTGCTATGATGAGCTTGAGTACCTGGAAATCATCTTAG 4320
 1414 K P N M V E A P E Q Y R F C Y D V A L E Y L E S * 1439

 4321 TTGGGTGAGACTCTTTAAGTCATCCATGAGAACCTGTTCCATCTATTGAGCCACCAAGCTGTTGACCTGTTAACCTT 4400
 4401 GTGCGAGAGATTTTAAATGCGGGGGTGGGAGACTTTACATTGAGAGGTTAAAGGTATTTTTTATGAAGTTTGAT 4480
 4481 CTTAATTAAGAAACTGAAACTGTTTTATTAATGATTAAGCATCAACATTGATCCACATTAAGGATTAATAATAA 4560
 4561 AGACCCAGATTGAAATGAGACGTTGGTTGTCAGTGAACATGCAACCTTTTCCATGGTTCAAGTAGCGAC 4640
 4641 TACCATGTT 4651

(SEQ ID NO: 4)

(SEQ ID NO: 2)

Fig. 15(3)

MCP7 HRPTP ₄	MDTTAAALPAFVALLLSEWELLGSAQCFSGAGCTPDDGACDYHQDLYDDPEWVHSAGEPHYLPPEDFOGSTHIV -HR LGTC - TL G -----TAAGT - L EPYST G S SEQ N EQ NTLTKPTSD W S LL	80 71
MCP7 HRPTP ₄	DSSDDEGEKARLQLPTMKENDTCIDPSYLVSQNLNPOTLNLRVNRNGPANTPTWNTGPTGRDWRALRMLAVSTEW NA GRPE CR H L OL H FVS KNSP L V V K N G IS DPT T N I	160 151
MCP7 HRPTP ₄	PNETWVPEAEVSGGSRGTAJADDIQLVSTPCDMSHFLALGOEVNAGCQATATGCAITATGDAVHNRLMORANGEDIV F V-TTS EQ L EVK GH THT ION F S I TVAGDR GIDVR A L	240 230
MCP7 HRPTP ₄	AQTNNMURERFAAEGTCACTTICDLCPTGTSOENGSGVNFNQALIVAFPRUJAPPQLOVGFTYLQIOMANSIIGD KEI VISS I NWNT R AGE MRT G V X Y E V K V A S A W N	320 310
MCP7 HRPTP ₄	GPIIIKEVEYRHTGGSWTHAVNPAKTXLHNLDPUETEIRVLLTRPGEGTGLPGPPLATRKAEPHRTFKTLKIAE VAR CTA NDQF DSTS EG S S AR D G RX EKV	400 390
MCP7 HRPTP ₄	XGARRIADWESLGINYINCHTCTENVYIYRCHGHH--SKADCLNDCEKAFCRNVRNHLPTTNSVLKHLINPREGRES VX5 Q TIR ET V SY L VH C QV QQ QVRENSH TENS TITH S V L M	478 470
MCP7 HRPTP ₄	ETIIILQEDDEVIGFVFTVSLQTSZENKJLFLNWNLKEDDPNGLLTOYEISTSSISSTDPAVFWAGCFTVSNUNSTHRYF OL V L A TEI STE E Q R TOT V L T KAVV EIDLNSNQRK K G E PL	558 550
MCP7 HRPTP ₄	MILHGTYGTOPIRATSTVGGFPATAINVITINASPLTBYEDVDSASINTTATTITVLLRPAQAKGAPISANQVRELM PG Y S T A EATQK S E A -LETP Q ON V K K H V V ER	638 629
MCP7 HRPTP ₄	PIHTRKEAGAMETCVGPFVTVNQAMSGAGPYAEEA---GILPERAPPTVCGNRTYQGPNNFPLAPKGTYNITYQAMSSYE R K ITTELL P HEI SLSNQ F ADA CAQ I K H Y T L Y S R A RAN	716 709
MCP7 HRPTP ₄	***** KETKQTQVLAHAKTANQVZPBDQXQGTRNVLMQXGELVFLILLVLLVLLVLLVLLVLLVLLVLLVLLVLLVLLVLLVLLV G ID QV G A-T KFV E E HT VI L VLF G V V R ET SS V	798 788
MCP7 HRPTP ₄	NAMDPSYADQSTILHAEDLGSTPHQDQHSTV-----EMISATASSRSLDWFY-LEE S K E G -NCDEB -- T LNS SVS265P7KSTLSTSPVNGTYPD T THASD S VQHT KKA	852 865
MCP7 HRPTP ₄	GTESPQQTQGQLHEAIRVADLQLRINLNMKTSTGPGREYEEPFECQGSASHVWKKQDNRAHNRYGMILAYDERSVILQW PAUV TQ CAEG P S E M R TI	932 945
MCP7 HRPTP ₄	EDDPQSYDINANNDYQGRSHTYATQGPVHETVYDNEWMNQEQGACIVKVVTRNLEV/GVHVKCYKMPDQTEVYGDPEV G TN G E N M Q I V H N N S I C I X I	1012 1025
MCP7 HRPTP ₄	CVEMERPLABTVVRLPTTLEPQYTMZLREVQFEPHTWQDIEGVYHATGILSPIRRNLNSP/SAGFIVVHCSCAGRTGZY LI T L I AV K VE IR G V O SKS L P	1092 1105
MCP7 HRPTP ₄	IVIDIMLDMAEERGVWDIYNYCVALRSRSGNQYTEROYTFIHDIALECLGEGAIAVCEPFRAXYDFMIRIDSQTSNSH RE V V D SV AZQVRSLY NKL P Q	1172 1185
MCP7 HRPTP ₄	LKDEFQTLNSVTPRLAQEDCSAICLARHMRPFRHMLPPDCRFLPLTIDGESSTYINALMDSYRQPAFIVTQTFPL I E R M T RV L E C X I K S H	1252 1265
MCP7 HRPTP ₄	NTVKDEWRLVYDGTCSIVMLVEVLDLSQCGQTYPEEGHNLRYGPIQVEDMSCSMDCDVDRIFRQNLTROPQGYLMVQO L H V D :PA L N VH H FV ADLER I S Y AA D R	1332 1345
MCP7 HRPTP ₄	POYLGWASHERVPGSKRSFLKLILQVENWCEEGGGTIIHCLNQGGRSGHRCAGIIVVEMVKHQVIVFHAVKTZR Y PMY DT V R D YNG P VV T S C LRH RT	1412 1425
MCP7 HRPTP ₄	NSKPNMVEAPEQTYCIVALEYLESS* N DLLD E N G*	1439 1452

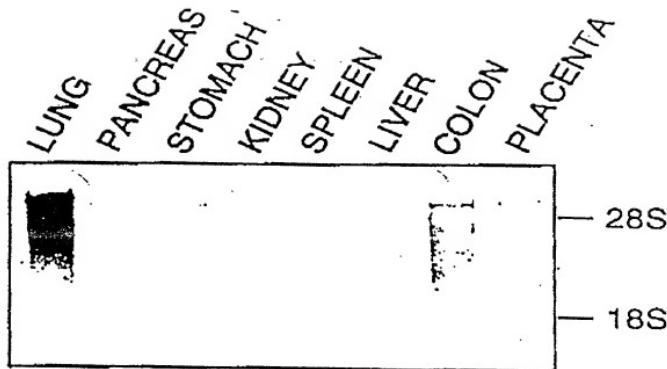


FIG. 17

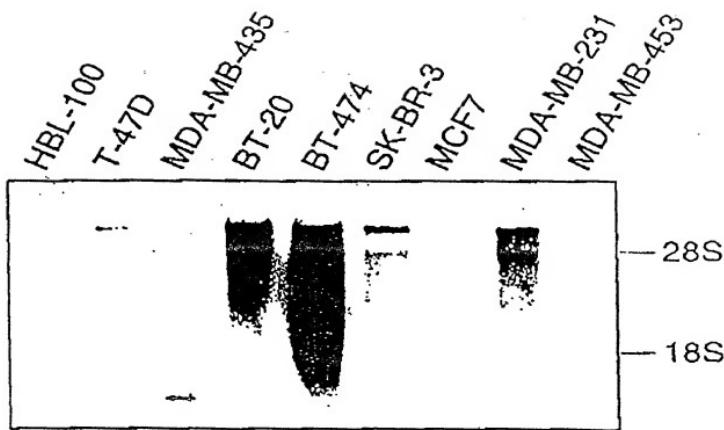


FIG. 18

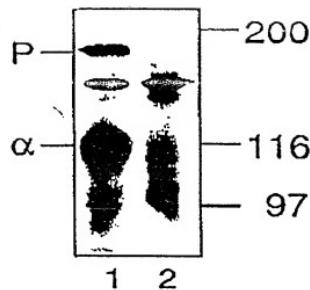
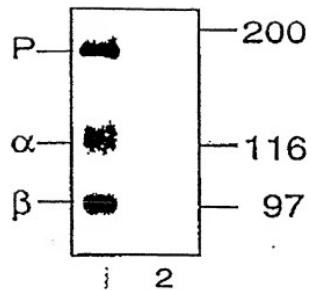


FIG. 19

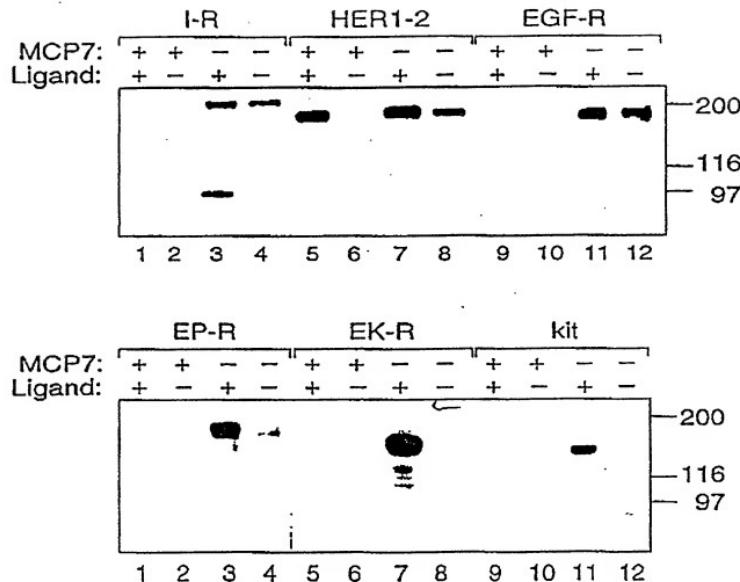


FIG. 20

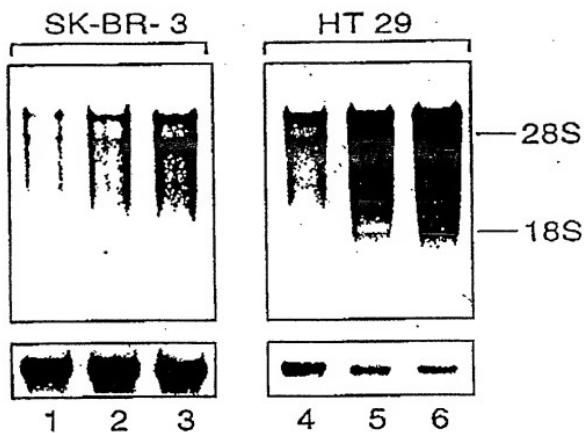


FIG. 21

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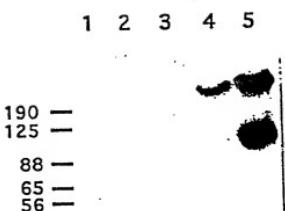


FIG. 22 A

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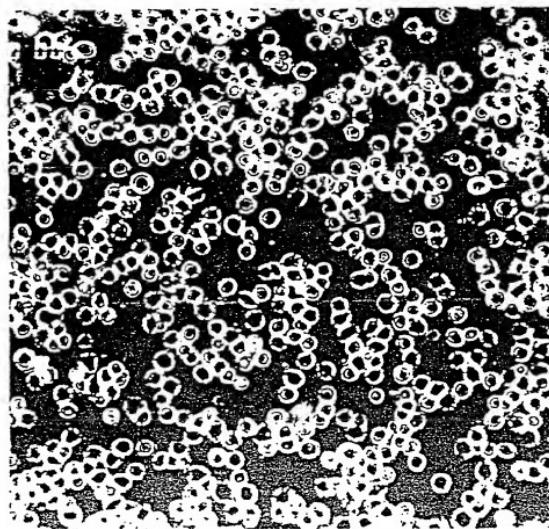
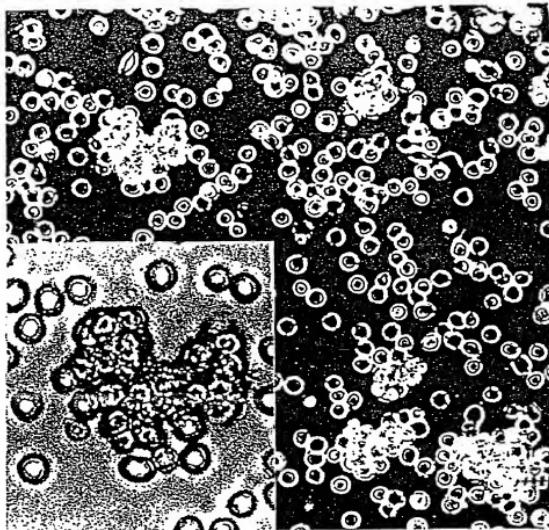


FIG. 22B

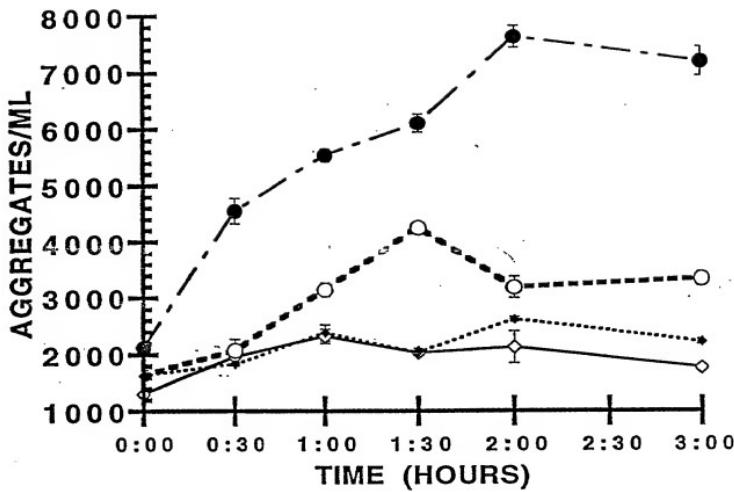


FIG. 22 C

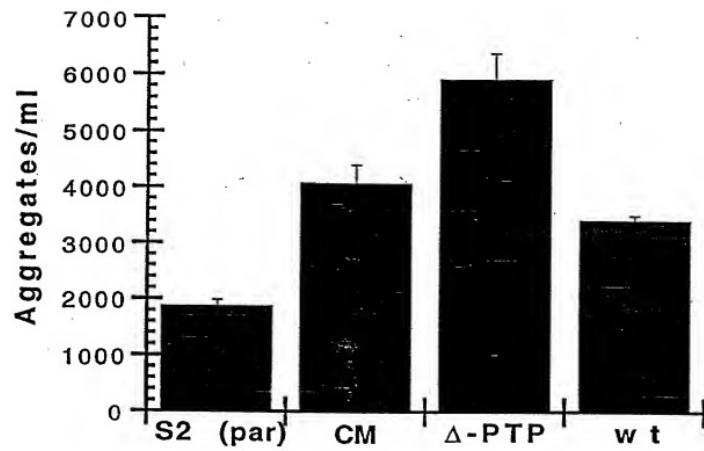
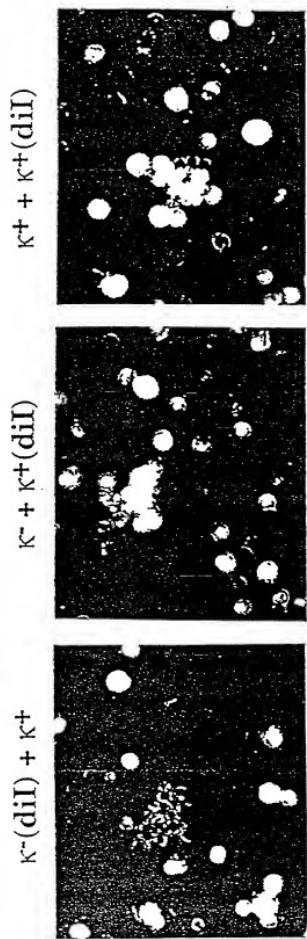


FIG. 22 D

FIG. 23



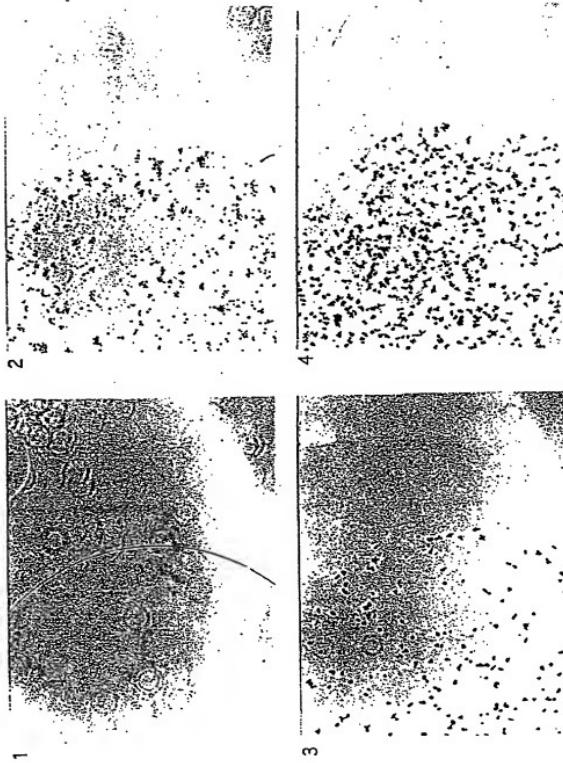


FIG. 24